

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 10/008,264B
Source: 1FW16
Date Processed by STIC: 7/29/05

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05



IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/008,264B

DATE: 07/29/2005
TIME: 08:03:58

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\07292005\J008264B.raw

3 <110> APPLICANT: Glimcher, Laurie H.
 4 Szabo, Susanne, J.
 6 <120> TITLE OF INVENTION: T-BET COMPOSITIONS AND METHODS OF USE THEREOF
 8 <130> FILE REFERENCE: HUI-040CP
 10 <140> CURRENT APPLICATION NUMBER: US 10/008264B
 11 <141> CURRENT FILING DATE: 2001-12-03
 13 <150> PRIOR APPLICATION NUMBER: PCT/US00/15345
 14 <151> PRIOR FILING DATE: 2000-06-01
 16 <150> PRIOR APPLICATION NUMBER: US 60/137085
 17 <151> PRIOR FILING DATE: 1999-06-02
 19 <160> NUMBER OF SEQ ID NOS: 9
 21 <170> SOFTWARE: PatentIn Ver. 2.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1608
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (1)..(1605)
 32 <400> SEQUENCE: 1
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 35 1 5 10 15
 37 ccg atg ccg ggg agc gac gag ggc cgg gct ggc gcc gac ccg cag 96
 38 Pro Met Pro Gly Ser Asp Glu Gly Arg Ala Pro Gly Ala Asp Pro Gln
 39 20 25 30
 41 cac cgc tac ttc tac ccg gag ccg ggc gcg cag gac gac gag cgt 144
 42 His Arg Tyr Phe Tyr Pro Glu Pro Gly Ala Gln Asp Ala Asp Glu Arg
 43 35 40 45
 45 cgc ggg ggc ggc agc ctg ggg tct ccc tac ccg ggg ggc gcc ttg gtg 192
 46 Arg Gly Gly Ser Leu Gly Ser Pro Tyr Pro Gly Gly Ala Leu Val
 47 50 55 60
 49 ccc gcc ccg ccg agc cgc ttc ctt gga gcc tac gcc tac ccg ccg cga 240
 50 Pro Ala Pro Pro Ser Arg Phe Leu Gly Ala Tyr Ala Tyr Pro Pro Arg
 51 65 70 75 80
 53 ccc cag gcg gcc ggc ttc ccc ggc gcg ggc gag tcc ttc ccg ccg ccc 288
 54 Pro Gln Ala Ala Gly Phe Pro Gly Ala Gly Glu Ser Phe Pro Pro Pro
 55 85 90 95
 57 gcg gac gcc gag ggc tac cag ccg ggc gag ggc tac gcc ggc ccg gac 336
 58 Ala Asp Ala Glu Gly Tyr Gln Pro Gly Glu Gly Tyr Ala Ala Pro Asp
 59 100 105 110
 62 ccg cgc gcc ggg ctc tac ccg ggg ccg cgt gag gac tac gcg cta ccc 384
 63 Pro Arg Ala Gly Leu Tyr Pro Gly Pro Arg Glu Asp Tyr Ala Leu Pro

*Does Not Comply
with Inserted Diskette Needs.*

JRC 6-7

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/008,264B

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Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\07292005\J008264B.raw

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66	gca gga ctg gag gtg tcg ggg aaa ctg agg gtc gcg ctc aac aac cac			432
67	Ala Gly Leu Glu Val Ser Gly Lys Leu Arg Val Ala Leu Asn Asn His			
68	130	135	140	
70	ctg ttg tgg tcc aag ttt aat cag cac cag aca gag atg atc atc acc			480
71	Leu Leu Trp Ser Lys Phe Asn Gln His Gln Thr Glu Met Ile Ile Thr			
72	145	150	155	160
74	aag cag gga cgg cgg atg ttc cca ttc ctg tca ttt act gtg gcc ggg			528
75	Lys Gln Gly Arg Arg Met Phe Pro Phe Leu Ser Phe Thr Val Ala Gly			
76	165	170	175	
78	ctg gag ccc acc agc cac tac agg atg ttt gtg gac gtg gtc ttg gtg			576
79	Leu Glu Pro Thr Ser His Tyr Arg Met Phe Val Asp Val Val Leu Val			
80	180	185	190	
82	gac cag cac cac tgg cgg tac cag agc ggc aag tgg gtg cag tgt gga			624
83	Asp Gln His His Trp Arg Tyr Gln Ser Gly Lys Trp Val Gln Cys Gly			
84	195	200	205	
86	aag gcc gag ggc agc atg cca gga aac cgc ctg tac gtc cac ccg gac			672
87	Lys Ala Glu Gly Ser Met Pro Gly Asn Arg Leu Tyr Val His Pro Asp			
88	210	215	220	
90	tcc ccc aac aca gga gcg cac tgg atg cgc cag gaa gtt tca ttt ggg			720
91	Ser Pro Asn Thr Gly Ala His Trp Met Arg Gln Glu Val Ser Phe Gly			
92	225	230	235	240
94	aaa cta aag ctc aca aac aag ggg gcg tcc aac aat gtg acc cag			768
95	Lys Leu Lys Leu Thr Asn Asn Lys Gly Ala Ser Asn Asn Val Thr Gln			
96	245	250	255	
98	atg att gtg ctc cag tcc ctc cat aag tac cag ccc cgg ctg cat atc			816
99	Met Ile Val Leu Gln Ser Leu His Lys Tyr Gln Pro Arg Leu His Ile			
100	260	265	270	
102	gtt gag gtg aac gac gga gag cca gag gca gcc tgc aac gct tcc aac			864
103	Val Glu Val Asn Asp Gly Glu Pro Glu Ala Ala Cys Asn Ala Ser Asn			
104	275	280	285	
106	acg cat atc ttt act ttc caa gaa acc cag ttc att gcc gtg act gcc			912
107	Thr His Ile Phe Thr Phe Gln Glu Thr Gln Phe Ile Ala Val Thr Ala			
108	290	295	300	
110	tac cag aat gcc gag att act cag ctg aaa att gat aat aac ccc ttt			960
111	Tyr Gln Asn Ala Glu Ile Thr Gln Leu Lys Ile Asp Asn Asn Pro Phe			
112	305	310	315	320
114	gcc aaa gga ttc cgg gag aac ttt gag tcc atg tac aca tct gtt gac			1008
115	Ala Lys Gly Phe Arg Glu Asn Phe Glu Ser Met Tyr Thr Ser Val Asp			
116	325	330	335	
118	acc agc atc ccc tcc ccg cct gga ccc aac tgt caa ttc ctt ggg gga			1056
119	Thr Ser Ile Pro Ser Pro Pro Gly Pro Asn Cys Gln Phe Leu Gly Gly			
120	340	345	350	
123	gat cac tac tct ctc cta ccc aac cag tat cct gtt ccc agc cgc			1104
124	Asp His Tyr Ser Pro Leu Leu Pro Asn Gln Tyr Pro Val Pro Ser Arg			
125	355	360	365	
127	ttc tac ccc gac ctt cct ggc cag gcg aag gat gtg gtt ccc cag gct			1152
128	Phe Tyr Pro Asp Leu Pro Gly Gln Ala Lys Asp Val Val Pro Gln Ala			
129	370	375	380	

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Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\07292005\J008264B.raw

131 tac tgg ctg ggg gcc ccc cg	gac cac agc tat gag gct gag ttt cga	1200
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133 385 390 395 400		
135 gca gtc agc atg aag cct gca ttc ttg ccc tct gcc cct ggg ccc acc		1248
136 Ala Val Ser Met Lys Pro Ala Phe Leu Pro Ser Ala Pro Gly Pro Thr		
137 405 410 415		
139 atg tcc tac tac cga ggc cag gag gtc ctg gca cct gga gct ggc tgg		1296
140 Met Ser Tyr Tyr Arg Gly Gln Glu Val Leu Ala Pro Gly Ala Gly Trp		
141 420 425 430		
143 cct gtg gca ccc cag tac cct ccc aag atg ggc ccg gcc agc tgg ttc		1344
144 Pro Val Ala Pro Gln Tyr Pro Pro Lys Met Gly Pro Ala Ser Trp Phe		
145 435 440 445		
147 cgc cct atg cgg act ctg ccc atg gaa ccc ggc cct gga ggc tca gag		1392
148 Arg Pro Met Arg Thr Leu Pro Met Glu Pro Gly Pro Gly Gly Ser Glu		
149 450 455 460		
151 gga cgg gga cca gag gac cag ggt ccc ccc ttg gtg tgg act gag att		1440
152 Gly Arg Gly Pro Glu Asp Gln Gly Pro Pro Leu Val Trp Thr Glu Ile		
153 465 470 475 480		
155 gcc ccc atc cgg ccg gaa tcc agt gat tca gga ctg ggc gaa gga gac		1488
156 Ala Pro Ile Arg Pro Glu Ser Ser Asp Ser Gly Leu Gly Glu Gly Asp		
157 485 490 495		
159 tct aag agg agg cgc gtg tcc ccc tat cct tcc agt ggt gac agc tcc		1536
160 Ser Lys Arg Arg Val Ser Pro Tyr Pro Ser Ser Gly Asp Ser Ser		
161 500 505 510		
163 tcc cct gct ggg gcc cct tct cct ttt gat aag gaa gct gaa gga cag		1584
164 Ser Pro Ala Gly Ala Pro Ser Pro Phe Asp Lys Glu Ala Glu Gly Gln		
165 515 520 525		
167 ttt tat aac tat ttt ccc aac tga		1608
168 Phe Tyr Asn Tyr Phe Pro Asn		
169 530 535		
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173 <211> LENGTH: 535		
174 <212> TYPE: PRT		
175 <213> ORGANISM: Homo sapiens		
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179 1 5 10 15		
181 Pro Met Pro Gly Ser Asp Glu Gly Arg Ala Pro Gly Ala Asp Pro Gln		
182 20 25 30		
184 His Arg Tyr Phe Tyr Pro Glu Pro Gly Ala Gln Asp Ala Asp Glu Arg		
185 35 40 45		
187 Arg Gly Gly Ser Leu Gly Ser Pro Tyr Pro Gly Gly Ala Leu Val		
188 50 55 60		
190 Pro Ala Pro Pro Ser Arg Phe Leu Gly Ala Tyr Ala Tyr Pro Pro Arg		
191 65 70 75 80		
193 Pro Gln Ala Ala Gly Phe Pro Gly Ala Gly Glu Ser Phe Pro Pro Pro		
194 85 90 95		
196 Ala Asp Ala Glu Gly Tyr Gln Pro Gly Glu Gly Tyr Ala Ala Pro Asp		
197 100 105 110		

RAW SEQUENCE LISTING

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TIME: 08:03:58

Input Set : A:\SEQUENCE LISTING.txt
 Output Set: N:\CRF4\07292005\J008264B.raw

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202 Ala Gly Leu Glu Val Ser Gly Lys Leu Arg Val Ala Leu Asn Asn His
203      130          135          140
205 Leu Leu Trp Ser Lys Phe Asn Gln His Gln Thr Glu Met Ile Ile Thr
206      145          150          155          160
208 Lys Gln Gly Arg Arg Met Phe Pro Phe Leu Ser Phe Thr Val Ala Gly
209      165          170          175
211 Leu Glu Pro Thr Ser His Tyr Arg Met Phe Val Asp Val Val Leu Val
212      180          185          190
214 Asp Gln His His Trp Arg Tyr Gln Ser Gly Lys Trp Val Gln Cys Gly
215      195          200          205
217 Lys Ala Glu Gly Ser Met Pro Gly Asn Arg Leu Tyr Val His Pro Asp
218      210          215          220
220 Ser Pro Asn Thr Gly Ala His Trp Met Arg Gln Glu Val Ser Phe Gly
221      225          230          235          240
223 Lys Leu Lys Leu Thr Asn Asn Lys Gly Ala Ser Asn Asn Val Thr Gln
224      245          250          255
226 Met Ile Val Leu Gln Ser Leu His Lys Tyr Gln Pro Arg Leu His Ile
227      260          265          270
229 Val Glu Val Asn Asp Gly Glu Pro Glu Ala Ala Cys Asn Ala Ser Asn
230      275          280          285
232 Thr His Ile Phe Thr Phe Gln Glu Thr Gln Phe Ile Ala Val Thr Ala
233      290          295          300
235 Tyr Gln Asn Ala Glu Ile Thr Gln Leu Lys Ile Asp Asn Asn Pro Phe
236      305          310          315          320
238 Ala Lys Gly Phe Arg Glu Asn Phe Glu Ser Met Tyr Thr Ser Val Asp
239      325          330          335
241 Thr Ser Ile Pro Ser Pro Pro Gly Pro Asn Cys Gln Phe Leu Gly Gly
242      340          345          350
245 Asp His Tyr Ser Pro Leu Leu Pro Asn Gln Tyr Pro Val Pro Ser Arg
246      355          360          365
248 Phe Tyr Pro Asp Leu Pro Gly Gln Ala Lys Asp Val Val Pro Gln Ala
249      370          375          380
251 Tyr Trp Leu Gly Ala Pro Arg Asp His Ser Tyr Glu Ala Glu Phe Arg
252      385          390          395          400
254 Ala Val Ser Met Lys Pro Ala Phe Leu Pro Ser Ala Pro Gly Pro Thr
255      405          410          415
257 Met Ser Tyr Tyr Arg Gly Gln Glu Val Leu Ala Pro Gly Ala Gly Trp
258      420          425          430
260 Pro Val Ala Pro Gln Tyr Pro Pro Lys Met Gly Pro Ala Ser Trp Phe
261      435          440          445
263 Arg Pro Met Arg Thr Leu Pro Met Glu Pro Gly Pro Gly Gly Ser Glu
264      450          455          460
266 Gly Arg Gly Pro Glu Asp Gln Gly Pro Pro Leu Val Trp Thr Glu Ile
267      465          470          475          480
269 Ala Pro Ile Arg Pro Glu Ser Ser Asp Ser Gly Leu Gly Glu Gly Asp
270      485          490          495
272 Ser Lys Arg Arg Val Ser Pro Tyr Pro Ser Ser Gly Asp Ser Ser

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RAW SEQUENCE LISTING
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DATE: 07/29/2005
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Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\07292005\J008264B.raw

273	500	505	510	
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289	<222> LOCATION: (1)..(1590)			
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296	ccg atg ccg agt gac gag ggc ccg ggg ccc gga gcg gac caa cag cat			96
297	Pro Met Pro Ser Asp Glu Gly Arg Gly Pro Gly Ala Asp Gln Gln His			
298	20 25 30			
300	cgt ttc ttc tat ccc gag ccg ggc gca cag gac ccg acc gat cgc cgc			144
301	Arg Phe Phe Tyr Pro Glu Pro Gly Ala Gln Asp Pro Thr Asp Arg Arg			
302	35 40 45			
306	gca ggt agc agc ctg ggg acg ccc tac tct ggg ggc gcc ctg gtg cct			192
307	Ala Gly Ser Ser Leu Gly Thr Pro Tyr Ser Gly Gly Ala Leu Val Pro			
308	50 55 60			
310	gcc gcg ccg ggt cgc ttc ctt gga tcc ttc gcc tac ccg ccc cgg gct			240
311	Ala Ala Pro Gly Arg Phe Leu Gly Ser Phe Ala Tyr Pro Pro Arg Ala			
312	65 70 75 80			
314	cag gtg gct ggc ttt ccc ggg cct ggc gag ttc ttc ccg ccg ccc gcg			288
315	Gln Val Ala Gly Phe Pro Gly Pro Glu Phe Phe Pro Pro Pro Ala			
316	85 90 95			
318	ggt gcg gag ggc tac ccg ccc gtg gat ggc tac cct gcc cct gac ccg			336
319	Gly Ala Glu Gly Tyr Pro Pro Val Asp Gly Tyr Pro Ala Pro Asp Pro			
320	100 105 110			
322	cgc gcg ggg ctc tac cca ggg ccg cgc gag gac tac gca ttg ccc gcg			384
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324	115 120 125			
326	ggg ttg gag gtg tct ggg aag ctg aga gtc gcg ctc agc aac cac ctg			432
327	Gly Leu Glu Val Ser Gly Lys Leu Arg Val Ala Leu Ser Asn His Leu			
328	130 135 140			
330	ttg tgg tcc aag ttc aac cag cac cag aca gag atg atc atc act aag			480
331	Leu Trp Ser Lys Phe Asn Gln His Gln Thr Glu Met Ile Ile Thr Lys			
332	145 150 155 160			
334	caa gga cgg cga atg ttc cca ttc ctg tcc ttc acc gtg gcc ggg ctg			528
335	Gln Gly Arg Arg Met Phe Pro Phe Leu Ser Phe Thr Val Ala Gly Leu			
336	165 170 175			
338	gag ccc aca agc cat tac agg atg ttt gtg gat gtg gtc ttg gtg gac			576
339	Glu Pro Thr Ser His Tyr Arg Met Phe Val Asp Val Val Leu Val Asp			
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10/08, 264B 6

needs explanation in 2207-2237
section

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<211> 27
<212> DNA
<213> Artificial Sequence

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<400> 7
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24

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24

<210> 9
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<212> DNA
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<400> 9
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24

Attorney Docket No.: HUI-040CP
10

delete

**RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/008,264B**

DATE: 07/29/2005
TIME: 08:03:59

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\07292005\J008264B.raw

Use of <220> Feature (NEW RULES) :

Sequence(s) are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or "Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:5, 6, 7, 8, 9

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/008,264B

DATE: 07/29/2005

TIME: 08:03:59

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\07292005\J008264B.raw

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L:546 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
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L:546 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:546
L:555 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>
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L:555 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
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L:563 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:7, <213>
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L:580 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:9, <213>
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L:580 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:580
L:584 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
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